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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/109,864

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This Raw Listing contains the General Information Section and up to first 5 pages.

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new format

1 <110> APPLICANT: Ni, Jian
 2 Gentz, Reiner
 3 Rosen, Craig A.
 4 Human Genome Sciences, Inc.
 5 <120> TITLE OF INVENTION: Galectin 11
 6 <130> FILE REFERENCE: PF354P1
 7 <140> CURRENT APPLICATION NUMBER: US/09/109,864
 8 <141> CURRENT FILING DATE: 1998-07-06
 9 <150> EARLIER APPLICATION NUMBER: 09/010,146
 10 <151> EARLIER FILING DATE: 1998-01-21
 11 <150> EARLIER APPLICATION NUMBER: 60/034,205
 12 <151> EARLIER FILING DATE: 1997-01-21
 13 <150> EARLIER APPLICATION NUMBER: 60/034,204
 14 <151> EARLIER FILING DATE: 1997-01-21
 15 <160> NUMBER OF SEQ ID NOS: 12
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO 1
 18 <211> LENGTH: 865
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 21 <400> SEQUENCE: 1
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 24 gtacggggac tggctctgca agagcgaag cattttactg tgagcctgag ggaccaggct 180
 25 gcccatgctc ctgtgacact cagggcctcc ttgcagaca gaactctggc ctggatctcc 240
 26 cgctgggggc agaagaaact gatctcagcc cccttctct tttaccccca gagattcttt 300
 27 gaggtgctgc tctgttcca ggaggagggg ctgaagctgg cgctcaatgg gcaggggctg 360
 28 ggggccacca gcatgaacca gcaggcctg gaggagctgc gggagctcg gatcagtga 420
 29 agtgtccagc tctactgtgt ccactcctga aggatggttc caggaaatac cgcagaaac 480
 30 aagagtcagc cactccccag ggccccactc tctccccctc attaaaccat ccacctgaac 540
 31 accagcacat cagggcctgg ttacacctg gggtcacgag actgagtcta caggagcttt 600
 32 gggcctgagg gaaggcacia gagggcaaag gttcctcgaa ctctgcacct tctccacca 660
 33 ggagcctggg atatggctcc atctgccttc agggcctgga ctgcactcac agaggcaagt 720
 34 gttgtagact aacaaagata ctccaaaata caatggctta aagaatgtgg tcatttatte 780
 35 tttattatth atttatttgt ggtcaaataa ataaataagg ttatttatth aaaaaaaaaa 840
 36 aaaaaaaaaa aaaaaaaaaa aaaaa 865
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 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
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 42 Met Ser Pro Arg Leu Glu Val Pro Cys Ser His Ala Leu Pro Gln Gly
 43 1 5 10 15
 44 Leu Ser Pro Gly Gln Val Ile Ile Val Arg Gly Leu Val Leu Gln Glu

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46  Pro Lys His Phe Thr Val Ser Leu Arg Asp Gln Ala Ala His Ala Pro
47          35          40          45
48  Val Thr Leu Arg Ala Ser Phe Ala Asp Arg Thr Leu Ala Trp Ile Ser
49          50          55          60
50  Arg Trp Gly Gln Lys Lys Leu Ile Ser Ala Pro Phe Leu Phe Tyr Pro
51          65          70          75          80
52  Gln Arg Phe Phe Glu Val Leu Leu Leu Phe Gln Glu Gly Gly Leu Lys
53          85          90          95
54  Leu Ala Leu Asn Gly Gln Gly Leu Gly Ala Thr Ser Met Asn Gln Gln
55          100          105          110
56  Ala Leu Glu Gln Leu Arg Glu Leu Arg Ile Ser Gly Ser Val Gln Leu
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58  Tyr Cys Val His Ser
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68      20          25          30
69  Ile Ser Gly Val Val Leu Ser Asp Ala Lys Arg Phe Gln Ile Asn Leu
70      35          40          45
71  Arg Cys Gly Gly Asp Ile Ala Phe His Leu Asn Pro Arg Phe Asp Glu
72      50          55          60
73  Asn Ala Val Val Arg Asn Thr Gln Ile Asn Asn Ser Trp Gly Pro Glu
74      65          70          75          80
75  Glu Arg Ser Leu Pro Gly Ser Met Pro Phe Ser Arg Gly Gln Arg Phe
76      85          90          95
77  Ser Val Trp Ile Leu Cys Glu Gly His Cys Phe Lys Val Ala Val Asp
78      100          105          110
79  Gly Gln His Ile Cys Glu Tyr Ser His Arg Leu Met Asn Leu Pro Asp
80      115          120          125
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83  Thr
84      145
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93      20          25          30
94  Ile Val Ile Arg Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val

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97          50          55          60
98  His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr
99          65          70          75          80
100 Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro
101          85          90          95
102 Phe Gln Lys Glu Lys Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys
103          100          105          110
104 Ala Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly
105          115          120          125
106 His Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys
107          130          135          140
108 Val Asn Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser
109          145          150          155          160
110 Thr Gln Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val
111          165          170          175
112 Pro Lys Ser Gly Thr Pro Gln Leu Arg Leu Pro Phe Ala Ala Arg Leu
113          180          185          190
114 Asn Thr Pro Met Gly Pro Gly Arg Thr Val Val Val Lys Gly Glu Val
115          195          200          205
116 Asn Ala Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala Gly Lys Ser
117          210          215          220
118 Lys Asp Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile Lys Ala Phe
119          225          230          235          240
120 Val Arg Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu Glu Arg Asn
121          245          250          255
122 Ile Thr Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu Met Ile Ile
123          260          265          270
124 Tyr Cys Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser
125          275          280          285
126 Leu Glu Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu
127          290          295          300
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131 <211> LENGTH: 30

132 <212> TYPE: DNA

133 <213> ORGANISM: Homo sapiens

134 <400> SEQUENCE: 5

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136 <210> SEQ ID NO 6

137 <211> LENGTH: 28

138 <212> TYPE: DNA

139 <213> ORGANISM: Homo sapiens

140 <400> SEQUENCE: 6

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143 <211> LENGTH: 32

144 <212> TYPE: DNA

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150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapiens
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156 <212> TYPE: DNA
157 <213> ORGANISM: Homo sapiens
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167 <211> LENGTH: 22
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169 <213> ORGANISM: Homo sapiens
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173 <211> LENGTH: 865
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177 <221> NAME/KEY: source
178 <222> LOCATION: Complement((1)..(865))
179 <223> OTHER INFORMATION: Reversed Complementary
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183      tggagtatct ttgttagtct acaacacttg cctctgtgag tgcagtccag gccctgaagg 180
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186      gtgaaccagg ccctgatgtg ctggtgttca ggtggatggt ttaatgaggg gaggagagtg 360
187      gggccctggg gagtggctga ctctgtttt ctgcggtatt tcctggaacc atccttcagg 420
188      agtggacaca gtagagctgg aacttccac tgatccggag ctccgcagc tgctccaggg 480
189      cctgctggtt catgctgggt gccccagcc cctgcccatt gagcgccagc ttcagccctc 540
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